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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/756,018ADATE: 03/29/2000  
TIME: 15:22:58

Input Set: H756018A.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1 <110> APPLICANT: Brian Seed  
2 Tara Pouyani  
3 <120> TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES  
4 AND METHODS  
5 <130> FILE REFERENCE: 00786/284002  
6 <140> CURRENT APPLICATION NUMBER: US/08/756,018A  
7 <141> CURRENT FILING DATE: 1996-11-25  
8 <150> EARLIER APPLICATION NUMBER: 60/000,213  
9 <151> EARLIER FILING DATE: 1995-06-14  
10 <150> EARLIER APPLICATION NUMBER: 08/661,960  
11 <151> EARLIER FILING DATE: 1996-06-12  
12 <160> NUMBER OF SEQ ID NOS: 17  
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20 1 5 10  
21 <210> SEQ ID NO 2  
22 <211> LENGTH: 16  
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27 1 5 10 15  
28 <210> SEQ ID NO 3  
29 <211> LENGTH: 42  
30 <212> TYPE: PRT  
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34 1 5 10 15  
35 Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp  
36 20 25 30  
37 Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro  
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39 <210> SEQ ID NO 4  
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41 <212> TYPE: PRT  
42 <213> ORGANISM: Homo sapiens  
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54                           20

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79	ggtgtccagt	cccaggtgca	gctggtgcag	tctggggctg	aggtgaagaa	gcctgggtcc	120
80	tcggtgaagg	tctcctgcaa	ggcttctgga	ggcaccttca	gcagctatgc	tatcagctgg	180
81	gtgcgacagg	cccctggaca	agggcttgag	tggatgggag	ggatcatccc	tatctttggt	240
82	acagcaaaact	acgcacagaa	gttcaggggc	agagtcacga	ttaccgcgga	cgaatccacg	300
83	agcacagcct	acatggagct	gagcagcctg	agatctgagg	acacggccgt	gtattactgt	360
84	gcgagagata	atggagcgta	ttgtagtggg	ggtagctgct	actcgggctg	gttcgacccc	420
85	tggggccagg	gaaccttggt	caccgtctct	tcaggtgagt	actgaattct	agctttcttg	480
86	ggcaggccag	gcctgacctt	ggctttgggg	cagggagggg	gctaagggtga	ggcagggtggc	540
87	gccagcaggt	gcacacccaa	tgcccatgag	cccagacact	ggacgctgaa	cctcgcggac	600
88	agttaagaac	ccaggggcct	ctgcgcctgg	gccagctct	gtcccacacc	gcggtcacat	660
89	ggcaccacct	ctcttgacgc	ctccaccaag	ggcccatcgg	tcttccccct	ggcaccctcc	720
90	tccaagagca	cctctggggg	cacagcggcc	ctgggctgcc	tggtcaagga	ctacttcccc	780
91	gaaccgggtga	cggtgtcgtg	gaactcaggc	gccctgacca	gcggcgtgca	caccttcccc	840
92	gctgtcctac	agtcctcagg	actctactcc	ctcagcagcg	tggtgaccgt	gccctccagc	900
93	agcttggggca	cccagaccta	catctgcaac	gtgaatcaca	agcccagcaa	caccaaggtg	960
94	gacaagaaag	ttggtgagag	gccagcacag	ggagggaggg	tgtctgctgg	aagcaggctc	1020

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97      tctggctttt tcccaggctc tgggcaggca caggctaggt gcccctaacc caggccctgc      1200
98      acacaaaggg gcaggtgctg ggctcagacc tgccaagagc catatccggg aggaccctgc      1260
99      ccctgaccta agcccacccc aaaggccaaa ctctccactc cctcagctcg gacaccttct      1320
100     ctccctcccag attccagtaa ctcccaatct tctctctgca gagcccaaat cttgtgacaa      1380
101     aactcacaca tgcccaccgt gcccaggtaa gccagcccag gcctcgccct ccagctcaag      1440
102     gcgggacagg tgccctagag tagcctgcat ccagggacag gcccagccg ggtgctgaca      1500
103     cgtccacctc catctcttcc tcagcacctg aactcctggg gggaccgtca gtcttcctct      1560
104     tccccccaaa acccaaggac accctcatga tctcccgga cctgaggtc acatgcgtgg      1620
105     tgggtggacgt gagccacgaa gacctgagg tcaagttcaa ctggtactg gacggcgtgg      1680
106     aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg taccgggtgg      1740
107     tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac aagtgcgaag      1800
108     tctccaacaa agccctccca gcccctatcg agaaaacat ctccaaagcc aaaggtggga      1860
109     cccgtggggg gcgagggcca catggacaga ggccggctcg gccaccctc tgccctgaga      1920
110     gtgaccgctg taccaacctc tgtcctacag ggcagccccg agaaccacag gtgtacaccc      1980
111     tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc ctggtcaaag      2040
112     gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg gagaacaact      2100
113     acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac agcaagctca      2160
114     ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg atgcatgagg      2220
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121     <400> SEQUENCE: 9

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124     Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly
125     20           25           30
126     Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
127     35           40           45
128     Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala
129     50           55           60
130     Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly
131     65           70           75           80
132     Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala
133     85           90           95
134     Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser
135     100          105          110
136     Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
137     115          120          125
138     Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
139     130          135          140
140     Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
141     145          150          155          160
142     Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
143     165          170          175
144     Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly

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145		180		185		190
146	Leu Tyr Ser	Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Asp Lys				
147		195		200		205
148	Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys					
149		210		215		220
150	Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro					
151		225		230		235
152	Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys					
153			245		250	255
154	Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp					
155		260		265		270
156	Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu					
157		275		280		285
158	Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu					
159		290		295		300
160	His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn					
161		305		310		315
162	Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly					
163			325		330	335
164	Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu					
165		340		345		350
166	Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr					
167		355		360		365
168	Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn					
169		370		375		380
170	Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe					
171		385		390		395
172	Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn					
173			405		410	415
174	Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr					
175		420		425		430
176	Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys					
177		435		440		

178 &lt;210&gt; SEQ ID NO 10

179 &lt;211&gt; LENGTH: 1894

180 &lt;212&gt; TYPE: DNA

181 &lt;213&gt; ORGANISM: Homo sapiens

182 &lt;400&gt; SEQUENCE: 10

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184	ccattgtgtg ccaacctagt accggtgcc atcaccaacg ccaccctgga ccagatcact	120
185	ggcaagtggg tttatatcgc atcggccttt cgaaacgagg agtacaataa gtcggttcag	180
186	gagatccaag caaccttctt ttacttcacc cccaacaaga cagaggacac gatctttctc	240
187	agagagtacc agacccgaca ggaccagtgc atctataaca ccacctacct gaatgtccag	300
188	cgggaaaatg ggaccatctc cagatacgtg ggaggccaag agcatttcgc tcaactgtctg	360
189	atcctcaggg acaccaagac ctacatgctt gcttttgacg tgaacgatga gaagaactgg	420
190	gggctgtctg tctatgctga caagccagag acgaccaagg agcaactggg agagttctac	480
191	gaagctctcg actgcttgcg cattcccaag tcagatgtcg tgtacaccga ttggaaaaag	540
192	gataagtgtg agccactgga gaagcagcac gagaaggaga ggaaacagga ggagggggaa	600
193	tcggatcccg aggggtgagta ctaagcttca gcgctcctgc ctggacgcat cccggctatg	660
194	cagccccagt ccagggcagc aaggcaggcc ccgtctgcct cttcacccgg agcctctgcc	720

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197      gccaagagcc atatccggga ggaccctgcc cctgacctaa gccaccccca aaggccaaac      900
198      tctccactcc ctcagctcgg acaccttctc tcctcccaga ttccagtaac tcccaatctt      960
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200      ccagcccagg cctcgccctc cagctcaagg cgggacaggt gccctagagt agcctgcatc     1080
201      cagggacagg ccccagccgg gtgtgacac gtccacctcc atctcttcct cagcacctga     1140
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204      caagttcaac tggtagctgg acggcggtgga ggtgcataat gccaaagaaa agccgcggga     1320
205      ggagcagtac aacagcacgt accgggtggt cagcgtcttc accgtcctgc accaggactg     1380
206      gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga     1440
207      gaaaaccatc tccaaagcca aagggtgggac ccgtgggggtg cgagggccac atggacagag     1500
208      gccggctcgg cccaccctct gccctgagag tgaccgtgt accaacctct gtcctacagg     1560
209      gcagccccga gaaccacagg tgtacaccct gcccctatcc cgggatgagc tgaccaagaa     1620
210      ccaggtcagc ctgacctgcc tggtaaagg cttctatccc agcgacatcg ccgtggagtg     1680
211      ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga     1740
212      cggctccttc ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa     1800
213      cgtcttctca tgctccgtga tgcagtggc tctgcacaac cactacacgc agaagagcct     1860
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&lt;210&gt; SEQ ID NO 11

&lt;211&gt; LENGTH: 437

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

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223      20              25              30
224      Asn Ala Thr Leu Asp Gln Ile Thr Gly Lys Trp Phe Tyr Ile Ala Ser
225      35              40              45
226      Ala Phe Arg Asn Glu Glu Tyr Asn Lys Ser Val Gln Glu Ile Gln Ala
227      50              55              60
228      Thr Phe Phe Tyr Phe Thr Pro Asn Lys Thr Glu Asp Thr Ile Phe Leu
229      65              70              75              80
230      Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile Tyr Asn Thr Thr Tyr
231      85              90              95
232      Leu Asn Val Gln Arg Glu Asn Gly Thr Ile Ser Arg Tyr Val Gly Gly
233      100             105             110
234      Gln Glu His Phe Ala His Leu Leu Ile Leu Arg Asp Thr Lys Thr Tyr
235      115             120             125
236      Met Leu Ala Phe Asp Val Asn Asp Glu Lys Asn Trp Gly Leu Ser Val
237      130             135             140
238      Tyr Ala Asp Lys Pro Glu Thr Thr Lys Glu Gln Leu Gly Glu Phe Tyr
239      145             150             155             160
240      Glu Ala Leu Asp Cys Leu Arg Ile Pro Lys Ser Asp Val Val Tyr Thr
241      165             170             175
242      Asp Trp Lys Lys Asp Lys Cys Glu Pro Leu Glu Lys Gln His Glu Lys
243      180             185             190
244      Glu Arg Lys Gln Glu Glu Gly Glu Ser Asp Pro Glu Gly Glu Pro Lys

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